08/430035

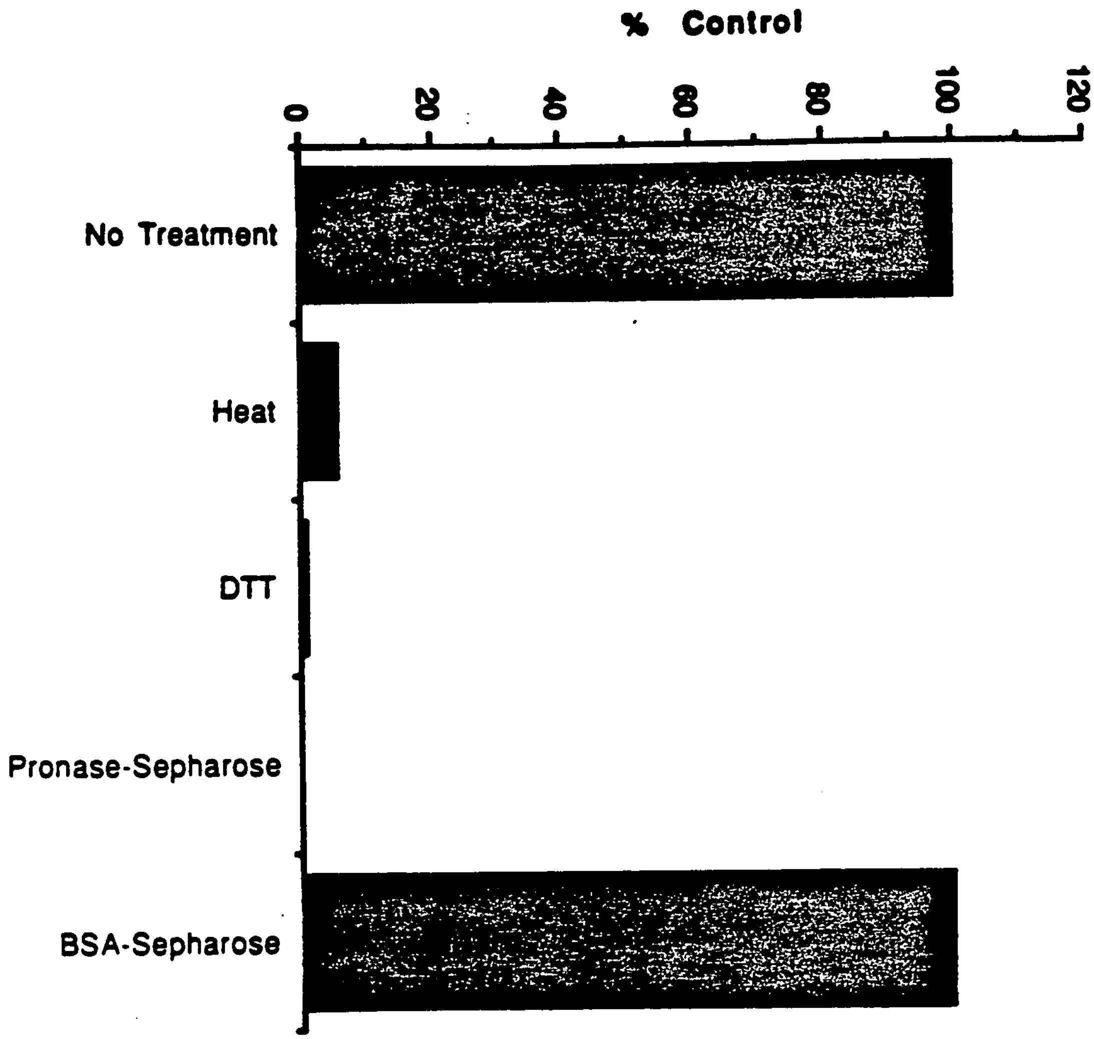

Figure 1

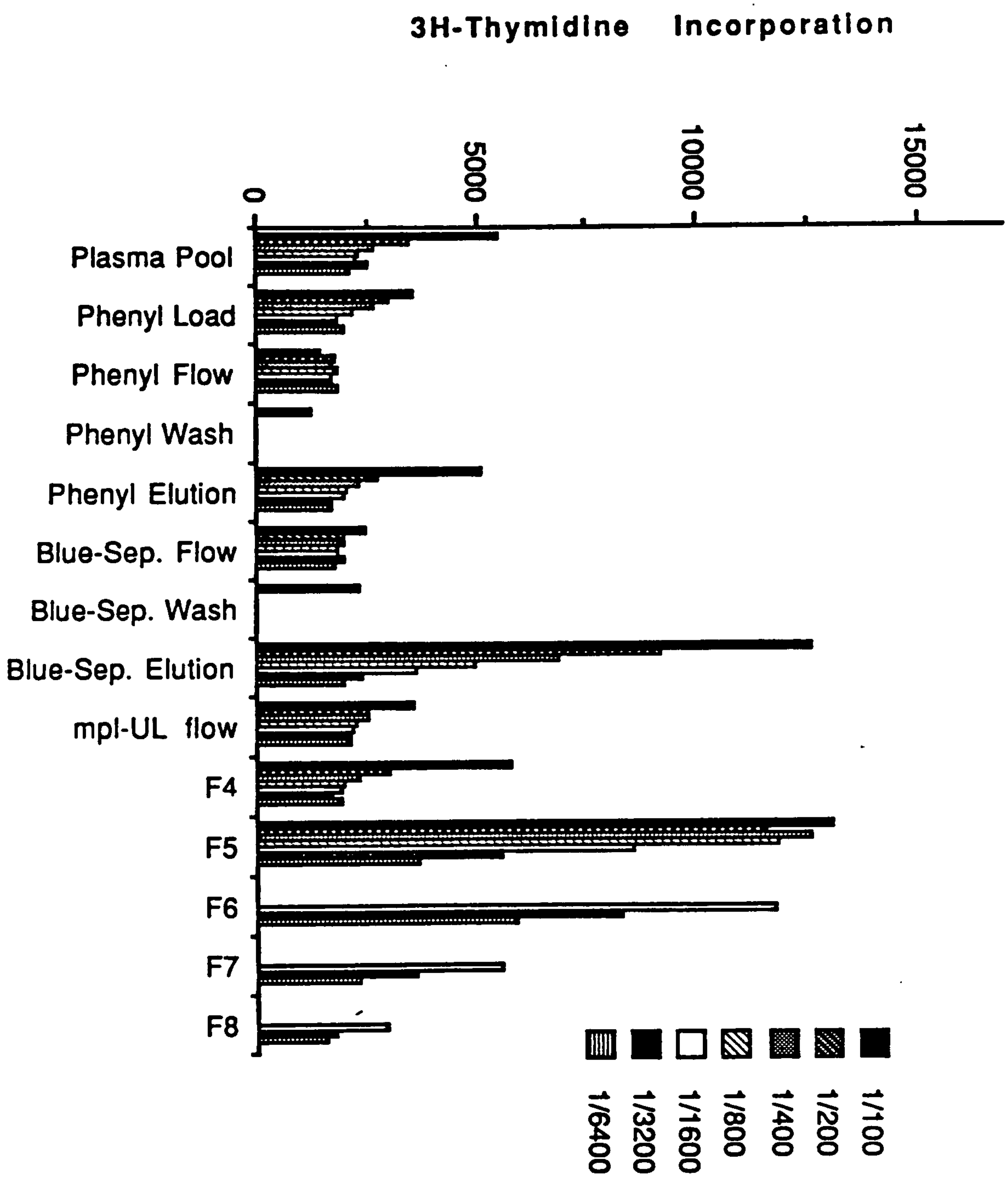
3H-Thymidine Incorporation
0
5000
10000
15000
Plasma Pool
Phenyl Load
Phenyl Flow
Phenyl Wash
Phenyl Elution
Blue-Sep. Flow
Blue-Sep. Wash
Blue-Sep. Elution
mpl-UL flow
F4
F5
F6
F7
F8
1/6400
1/3200
1/1600
1/800
1/400
1/200
1/100

Figure 2

08/430035

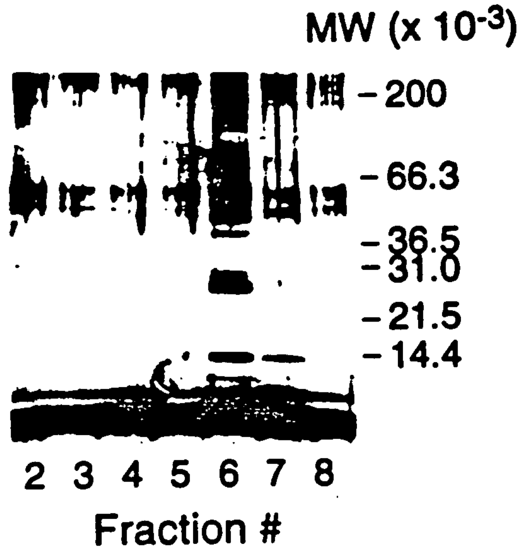

Figure 3

08/430035

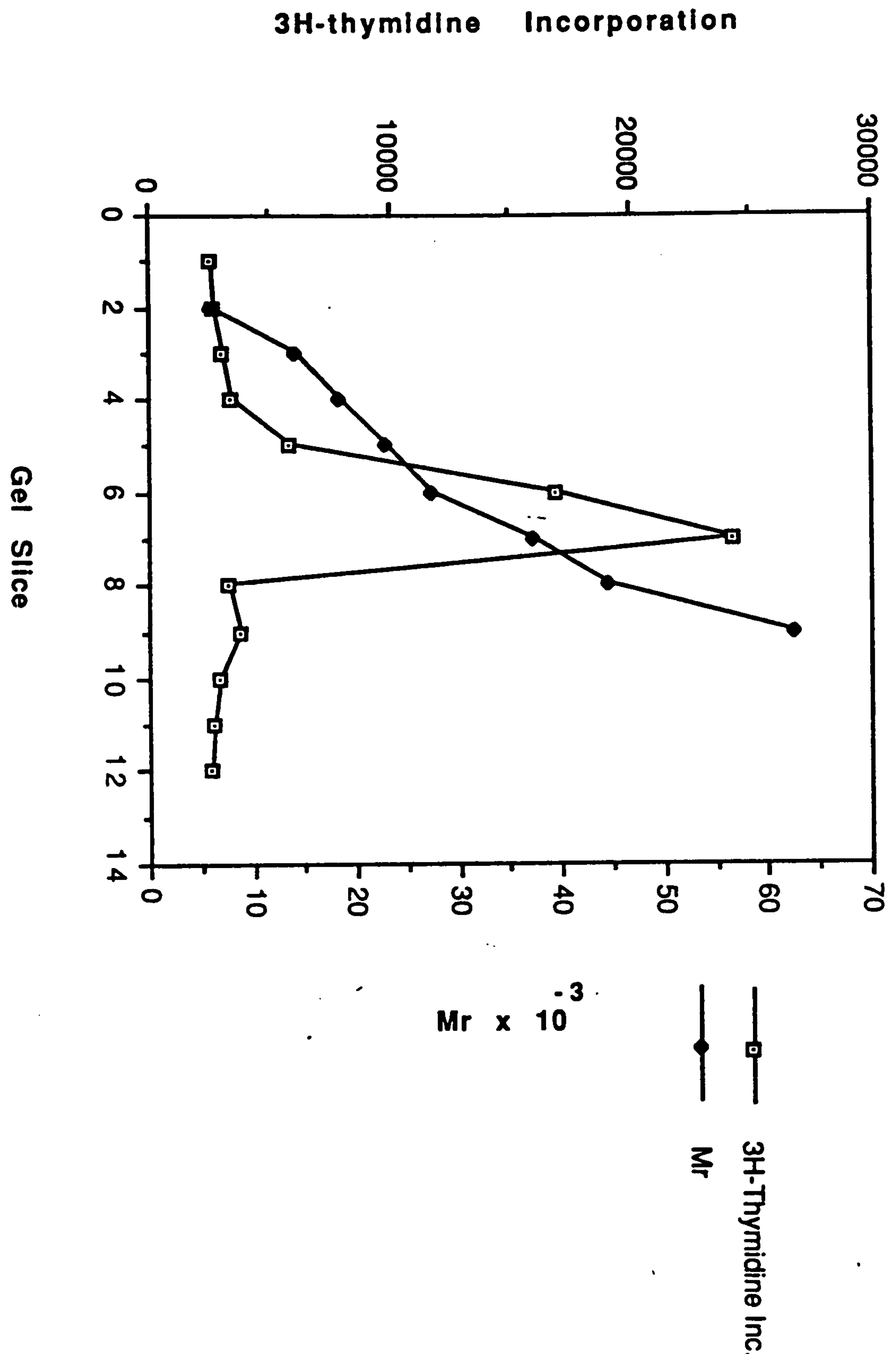

Figure 4

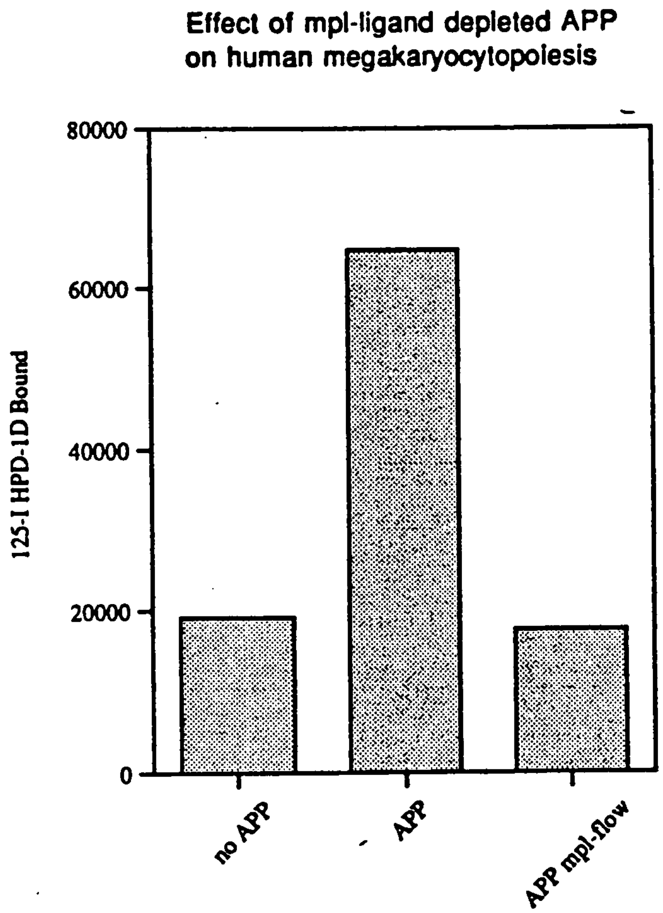
Effect of mpl-ligand depleted APP
on human megakaryocytopoiesis
80000
60000
40000
20000
0
125-I HPD-1D Bound
no APP
APP
APP mpl-flow

Figure 5

08/430035

125I-HP1-1D Bound

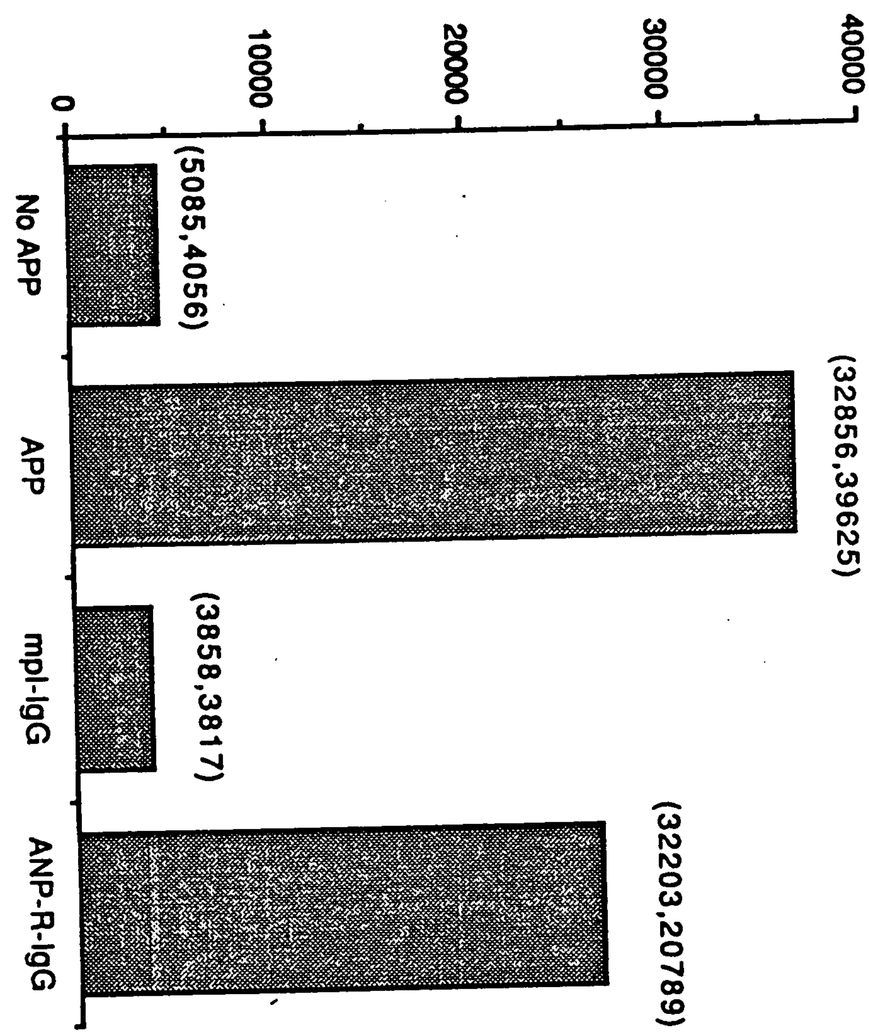

Figure 6

```
                                                                                                       -10
                                                                        ↓  L  L  L  V    V  M  L    L  L  T
  1 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT
    CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA

                                                  10                                 20
    A  R  L  T    L  S  S    P  A  P    P  A  C  D    L  R  V    L  S  K    L  L  R  D    S  H  V    L  H  S    R  L ↓
101 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
    CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT

201 GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT
    CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA

301 TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA
    AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT
```

Figure 7

08/430035

```
  1 GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCT TGGCCCGCCT
    CGCAGAAGGA TGGGTAGACG AGGGGTCTCC CGACGGACGA CACGTGAACC CAGGACCTCG GGAAGAGGTG GGCCTATCTA AGGAGTGGGA ACCGGGCGGA

101 TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT GGCCCCAGGA AGGATTCAGG GGAGAGGCCC CAAACAGGGA GCCACGCCAG
    AACGGGGTGG GATGAGACGG GTCTTCACGT TCTCGGATTC GGCGGAGGTA CCGGGGTCCT TCCTAAGTCC CCTCTCCGGG GTTTGTCCCT CGGTGCGGTC

                          -20                           -10                                      1
                       Me tGluLeuThr GluLeuLeuL euValValMe tLeuLeuLeu ThrAlaArgL euThrLeuSe rSerProAla ProProAlaCys
201 CCAGACACCC CGGCCAGAAT GGAGCTGACT GAATTGCTCC TCGTGGTCAT GCTTCTCCTA ACTGCAAGGC TAACGCTGTC CAGCCCGGCT CCTCCTGCTT
    GGTCTGTGGG GCCGGTCTTA CCTCGACTGA CTTAACGAGG AGCACCAGTA CGAAGAGGAT TGACGTTCCG ATTGCGACAG GTCGGGCCGA GGAGGACGAA

            10                      20                          30                                     40
 AspLeuAr gValLeuSer LysLeuLeuA rgAspSerHi sValLeuHis SerArgLeuS erGlnCysPr oGluValHis ProLeuProT hrProValLeu
301 GTGACCTCCG AGTCCTCAGT AAACTGCTTC GTGACTCCCA TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTCAC CCTTTGCCTA CACCTGTCCT
    CACTGGAGGC TCAGGAGTCA TTTGACGAAG CACTGAGGGT ACAGGAAGTG TCGTCTGACT CGGTCACGGG TCTCCAAGTG GGAAACGGAT GTGGACAGGA

                                 50                          60                          70
  LeuProAla ValAspPheS erLeuGlyGl uTrpLysThr GlnMetGluG luThrLysAl aGlnAspIle LeuGlyAlaV alThrLeuLe uLeuGluGly
401 GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA
    CGACGGACGA CACCTGAAAT CGAACCCTCT TACCTTTTGG GTCTACCTCC TCTGGTTCCG TGTCCTGTAA GACCCTCGTC ACTGGGAAGA CGACCTCCCT

                      80                          90                          100
    ValMetAlaA laArgGlyGl nLeuGlyPro ThrCysLeuS erSerLeuLe uGlyGlnLeu SerGlyGlnV alArgLeuLe uLeuGlyAla LeuGlnSerLeu
501 GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC
    CACTACCGTC GTGCCCCTGT TGACCCTGGG TGAACGGAGA GTAGGGAGGA CCCCGTCGAA AGACCTGTCC AGGCAGAGGA GGAACCCCGG GACGTCTCGG

           110                     120                         130                                     140
  LeuGlyTh rGlnLeuPro ProGlnGlyA rgThrThrAl aHisLysAsp ProAsnAlaI lePheLeuSe rPheGlnHis LeuLeuArgG lyLysValArg
601 TCCTTGGAAC CCAGCTTCCT CCACAGGGCA GGACCACAGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC CTGCTCCGAG GAAAGGTGCG
    AGGAACCTTG GGTCGAAGGA GGTGTCCCGT CCTGGTGTCG AGTGTTCCTA GGGTTACGGT AGAAGGACTC GAAGGTTGTG GACGAGGCTC CTTTCCACGC

                                 150                         160                         170
  PheLeuMet LeuValGlyG lySerThrLe uCysValArg ArgAlaProP roThrThrAl aValProSer ArgThrSerL euValLeuTh rLeuAsnGlu
701 TTTCCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG CGGGCCCCAC CCACCACAGC TGTCCCCAGC AGAACCTCTC TAGTCCTCAC ACTGAACGAG
    AAAGGACTAC GAACATCCTC CCAGGTGGGA GACGCAGTCC GCCCGGGGTG GGTGGTGTCG ACAGGGGTCG TCTTGGAGAG ATCAGGAGTG TGACTTGCTC

                      180                          190                          200
    LeuProAsnA rgThrSerGl yLeuLeuGlu ThrAsnPheT hrAlaSerAl aArgThrThr GlySerGlyL euLeuLysTr pGlnGlnGly PheArgAlaLys
801 CTCCCAAACA GGACTTCTGG ATTGTTGGAG ACAAACTTCA CTGCCTCAGC CAGAACTACT GGCTCTGGGC TTCTGAAGTG GCAGCAGGGA TTCAGAGCCA
    GAGGGTTTGT CCTGAAGACC TAACAACCTC TGTTTGAAGT GACGGAGTCG GTCTTGATGA CCGAGACCCG AAGACTTCAC CGTCGTCCCT AAGTCTCGGT
```

Figure 8a

```
            210                                      220                                      230                                      240
       IleProGl yLeuLeuAsn GlnThrSerA rgSerLeuAs pGlnIlePro GlyTyrLeuA snArgIleHi sGluLeuLeu AsnGlyThrA rgGlyLeuPhe
 901 AGATTCCTGG TCTGCTGAAC CAAACCTCCA GGTCCCTGGA CCAAATCCCC GGATACCTGA ACAGGATACA CGAACTCTTG AATGGAACTC GTGGACTCTT
     TCTAAGGACC AGACGACTTG GTTTGGAGGT CCAGGGACCT GGTTTAGGGG CCTATGGACT TGTCCTATGT GCTTGAGAAC TTACCTTGAG CACCTGAGAA

                                  250                                      260                                      270
       ProGlyPro SerArgArgT hrLeuGlyAl aProAspIle SerSerGlyT hrSerAspTh rGlySerLeu ProProAsnL euGlnProGl yTyrSerPro
1001 TCCTGGACCC TCACGCAGGA CCCTAGGAGC CCCGGACATT TCCTCAGGAA CATCAGACAC AGGCTCCCTG CCACCCAACC TCCAGCCTGG ATATTCTCCT
     AGGACCTGGG AGTGCGTCCT GGGATCCTCG GGGCCTGTAA AGGAGTCCTT GTAGTCTGTG TCCGAGGGAC GGTGGGTTGG AGGTCGGACC TATAAGAGGA

                       280                                      290                                      300
     SerProThrH isProProTh rGlyGlnTyr ThrLeuPheP roLeuProPr oThrLeuPro ThrProValV alGlnLeuHi sProLeuLeu ProAspProSer
1101 TCCCCAACCC ATCCTCCTAC TGGACAGTAT ACGCTCTTCC CTCTTCCACC CACCTTGCCC ACCCCTGTGG TCCAGCTCCA CCCCCTGCTT CCTGACCCTT
     AGGGGTTGGG TAGGAGGATG ACCTGTCATA TGCGAGAAGG GAGAAGGTGG GTGGAACGGG TGGGGACACC AGGTCGAGGT GGGGGACGAA GGACTGGGAA

            310                                      320                                      330
      AlaProTh rProThrPro ThrSerProL euLeuAsnTh rSerTyrThr HisSerGlnA snLeuSerGl nGluGly
1201 CTGCTCCAAC GCCCACCCCT ACCAGCCCTC TTCTAAACAC ATCCTACACC CACTCCCAGA ATCTGTCTCA GGAAGGGTAA GGTTCTCAGA CACTGCCGAC
     GACGAGGTTG CGGGTGGGGA TGGTCGGGAG AAGATTTGTG TAGGATGTGG GTGAGGGTCT TAGACAGAGT CCTTCCCATT CCAAGAGTCT GTGACGGCTG

1301 ATCAGCATTG TCTCATGTAC AGCTCCCTTC CCTGCAGGGC GCCCCTGGGA GACAACTGGA CAAGATTTCC TACTTTCTCC TGAAACCCAA AGCCCTGGTA
     TAGTCGTAAC AGAGTACATG TCGAGGGAAG GGACGTCCCG CGGGGACCCT CTGTTGACCT GTTCTAAAGG ATGAAAGAGG ACTTTGGGTT TCGGGACCAT

1401 AAAGGGATAC ACAGGACTGA AAAGGGAATC ATTTTTCACT GTACATTATA AACCTTCAGA AGCTATTTTT TTAAGCTATC AGCAATACTC ATCAGAGCAG
     TTTCCCTATG TGTCCTGACT TTTCCCTTAG TAAAAAGTGA CATGTAATAT TTGGAAGTCT TCGATAAAAA AATTCGATAG TCGTTATGAG TAGTCTCGTC

1501 CTAGCTCTTT GGTCTATTTT CTGCAGAAAT TTGCAACTCA CTGATTCTCT ACATGCTCTT TTTCTGTGAT AACTCTGCAA AGGCCTGGGC TGGCCTGGCA
     GATCGAGAAA CCAGATAAAA GACGTCTTTA AACGTTGAGT GACTAAGAGA TGTACGAGAA AAAGACACTA TTGAGACGTT TCCGGACCCG ACCGGACCGT

1601 GTTGAACAGA GGGAGAGACT AACCTTGAGT CAGAAAACAG AGAAAGGGTA ATTTCCTTTG CTTCAAATTC AAGGCCTTCC AACGCCCCCA TCCCCTTTAC
     CAACTTGTCT CCCTCTCTGA TTGGAACTCA GTCTTTTGTC TCTTTCCCAT TAAAGGAAAC GAAGTTTAAG TTCCGGAAGG TTGCGGGGGT AGGGGAAATG

1701 TATCATTCTC AGTGGGACTC TGATCCCATA TTCTTAACAG ATCTTTACTC TTGAGAAATG AATAAGCTTT CTCTCAGAAA AAAAAAAAAA AAAAAAA
     ATAGTAAGAG TCACCCTGAG ACTAGGGTAT AAGAATTGTC TAGAAATGAG AACTCTTTAC TTATTCGAAA GAGAGTCTTT TTTTTTTTTT TTTTTTT
```

Figure 8b

```
hmpl1   1   - - - - - - M E L T E L L L V V M L L L T A R L T L S S P A P P A C D L R V L S K L L R D S H V L H
hepo    1   M G V H E C P A W L W L L L S L L S L P L G L P V L G A P P R L I C D S R V L E R Y L L E A K E A E

hmpl1   45  S R L S Q C P E V H P L P T P V L L P A V D F S L G E W K T Q M E E T K A Q D I L G A V T L L L E G
hepo    51  N I T T G C A E H C S L N E N I T V P D T K V N F Y A W K R M E V G Q Q A V E V W Q G L A L L S E A

hmpl1   95  V M A A R G Q L G P T C L S - - S L L G Q L S G Q V R L L - - L G A L Q S L L G T Q - - - L P P Q G
hepo    101 V L R G Q A L L V N S S Q P W E P L Q L H V D K A V S G L R S L T T L L R A L G A Q K E A I S P P D

hmpl1   138 R T T A H K D P N A I F L S F Q H L L R G K V R F L - - - M L V G G S T L C V R R A P P T T A V P S
hepo    151 A A S A A P L R T I T A D T F R K L F R V Y S N F L R G K L K L Y T G E A C R T G D R

hmpl1   185 R T S L V L T L N E L P N R T S G L L E T N F T A S A R T T G S G L L K W Q Q G F R A K I P G L L N

hmpl1   235 Q T S R S L D Q I P G Y L N R I H E L L N G T R G L F P G P S R R T L G A P D I S S G T S D T G S L

hmpl1   285 P P N L Q P G Y S P S P T H P P T G Q Y T L F P L P P T L P T P V V Q L H P L L P D P S A P T P T P

hmpl1   335 T S P L L N T S Y T H S Q N L S Q E G
```

Figure 9

Proliferation Assay

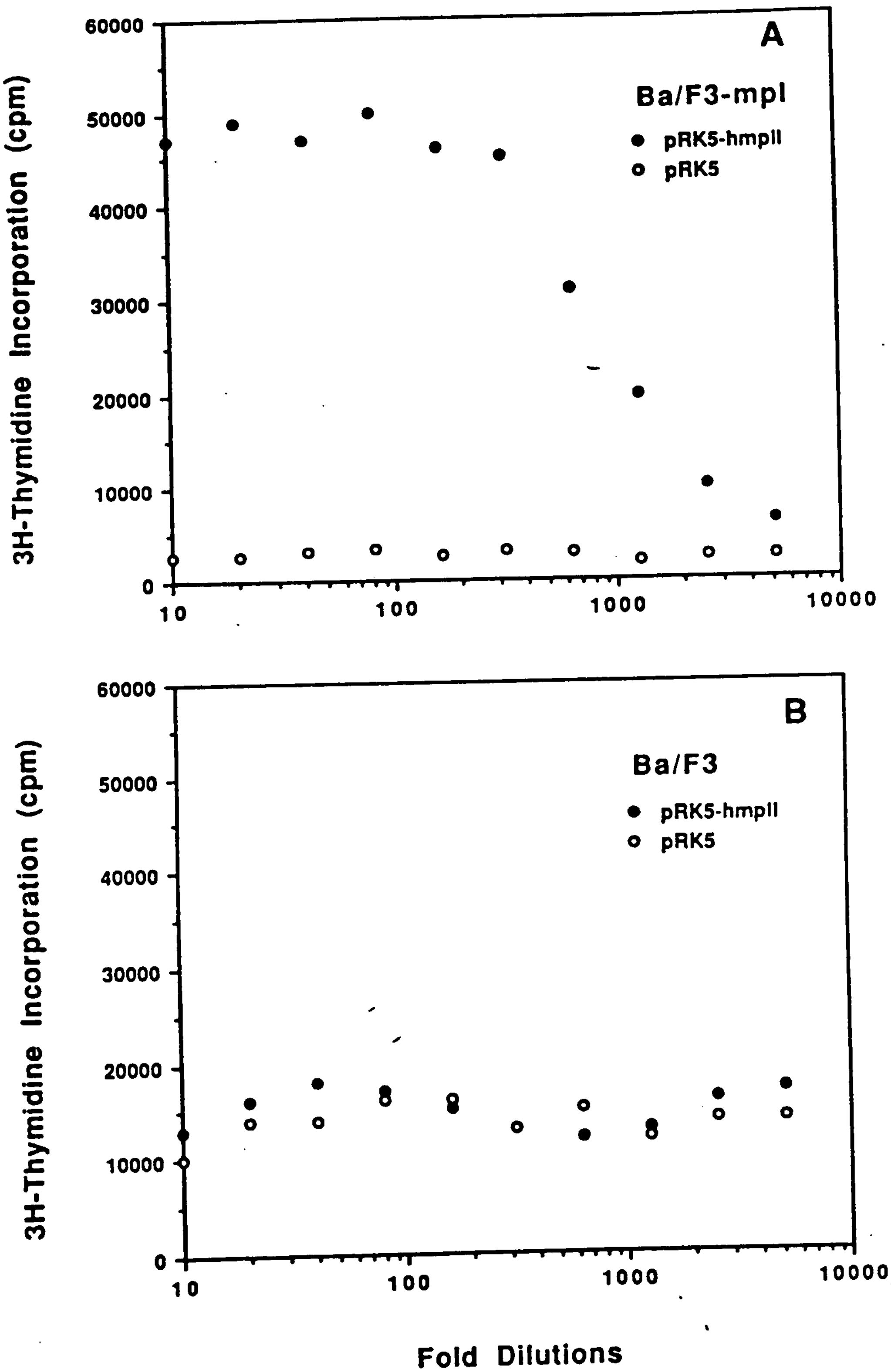

Figure 10